

SEQUENCE LISTING

<110> Weaver, Lynne

<120> METHODS OF TREATING CHRONIC PAIN USING COMPOSITIONS THAT SPECIFICALLY BIND CD11D (ALPHA-D) INTEGRIN

<130> 27866/39702

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 3726

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3) ..(3485)

<223>

<400> 1	47
tg acc ttc ggc act gtg ctt ctt ctg agt gtc ctg gct tct tat cat	
Thr Phe Gly Thr Val Leu Leu Leu Ser Val Leu Ala Ser Tyr His	
1 5 10 15	
gga ttc aac ctg gat gtg gag gag cct acg atc ttc cag gag gat gca	95
Gly Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala	
20 25 30	
ggc ggc ttt ggg cag agc gtg gtg cag ttc ggt gga tct cga ctc gtg	143
Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg Leu Val	
35 40 45	
gtg gga gca ccc ctg gag gtg gtg gcg gcc aac cag acg gga cgg ctg	191
Val Gly Ala Pro Leu Glu Val Val Ala Ala Asn Gln Thr Gly Arg Leu	
50 55 60	
tat gac tgc gca gct gcc acc ggc atg tgc cag ccc atc ccg ctg cac	239
Tyr Asp Cys Ala Ala Ala Thr Gly Met Cys Gln Pro Ile Pro Leu His	
65 70 75	
atc cgc cct gag gcc gtg aac atg tcc ttg ggc ctg acc ctg gca gcc	287
Ile Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala	
80 85 90 95	
tcc acc aac ggc tcc cgg ctc ctg gcc tgt ggc ccg acc ctg cac aga	335
Ser Thr Asn Gly Ser Arg Leu Leu Ala Cys Gly Pro Thr Leu His Arg	
100 105 110	
gtc tgt ggg gag aac tca tac tca aag ggt tcc tgc ctc ctg ctg ggc	383
Val Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu Gly	
115 120 125	
tcg cgc tgg gag atc atc cag aca gtc ccc gac gcc acg cca gag tgt	431
Ser Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro Glu Cys	
130 135 140	

cca cat caa gag atg gac atc gtc ttc ctg att gac ggc tct gga agc Pro His Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser 145 150 155	479
att gac caa aat gac ttt aac cag atg aag ggc ttt gtc caa gct gtc Ile Asp Gln Asn Asp Phe Asn Gln Met Lys Gly Phe Val Gln Ala Val 160 165 170 175	527
atg ggc cag ttt gag ggc act gac acc ctg ttt gca ctg atg cag tac Met Gly Gln Phe Glu Gly Thr Asp Thr Leu Phe Ala Leu Met Gln Tyr 180 185 190	575
tca aac ctc ctg aag atc cac ttc acc ttc acc caa ttc cgg acc agc Ser Asn Leu Leu Lys Ile His Phe Thr Phe Thr Gln Phe Arg Thr Ser 195 200 205	623
ccg agc cag cag agc ctg gtg gat ccc atc gtc caa ctg aaa ggc ctg Pro Ser Gln Gln Ser Leu Val Asp Pro Ile Val Gln Leu Lys Gly Leu 210 215 220	671
acg ttc acg gcc acg ggc atc ctg aca gtg gtg aca cag cta ttt cat Thr Phe Thr Ala Thr Gly Ile Leu Thr Val Val Thr Gln Leu Phe His 225 230 235	719
cat aag aat ggg gcc cga aaa agt gcc aag aag atc ctc att gtc atc His Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile Val Ile 240 245 250 255	767
aca gat ggg cag aag tac aaa gac ccc ctg gaa tac agt gat gtc atc Thr Asp Gly Gln Lys Tyr Lys Asp Pro Leu Glu Tyr Ser Asp Val Ile 260 265 270	815
ccc cag gca gag aag gct ggc atc atc cgc tac gct atc ggg gtg gga Pro Gln Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly 275 280 285	863
cac gct ttc cag gga ccc act gcc agg cag gag ctg aat acc atc agc His Ala Phe Gln Gly Pro Thr Ala Arg Gln Glu Leu Asn Thr Ile Ser 290 295 300	911
tca gcg cct ccg cag gac cac gtg ttc aag gtg gac aac ttt gca gcc Ser Ala Pro Pro Gln Asp His Val Phe Lys Val Asp Asn Phe Ala Ala 305 310 315	959
ctt ggc agc atc cag aag cag ctg cag gag aag atc tat gca gtt gag Leu Gly Ser Ile Gln Lys Gln Leu Gln Glu Lys Ile Tyr Ala Val Glu 320 325 330 335	1007
gga acc cag tcc agg gca agc agc tcc ttc cag cac gag atg tcc caa Gly Thr Gln Ser Arg Ala Ser Ser Phe Gln His Glu Met Ser Gln 340 345 350	1055
gaa ggc ttc agc aca gcc ctc aca atg gat ggc ctc ttc ctg ggg gct Glu Gly Phe Ser Thr Ala Leu Thr Met Asp Gly Leu Phe Leu Gly Ala 355 360 365	1103
gtg ggg agc ttt agc tgg tct gga ggt gcc ttc ctg tat ccc cca aat Val Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn 370 375 380	1151
atg agc ccc acc ttc atc aac atg tct cag gag aat gtg gac atg agg Met Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg 385 390 395	1199

gac tct tac ctg ggt tac tcc acc gag cta gcc ctg tgg aag ggg gta	1247
Asp Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly Val	
400 405 410 415	
cag aac ctg gtc ctg ggg gcc ccc cgc tac cag cat acc ggg aag gct	1295
Gln Asn Leu Val Leu Gly Ala Pro Arg Tyr Gln His Thr Gly Lys Ala	
420 425 430	
gtc atc ttc acc cag gtg tcc agg caa tgg agg aag aag gcc gaa gtc	1343
Val Ile Phe Thr Gln Val Ser Arg Gln Trp Arg Lys Lys Ala Glu Val	
435 440 445	
aca ggg acg cag atc ggc tcc tac ttc ggg gcc tcc ctc tgc tcc gtg	1391
Thr Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val	
450 455 460	
gat gtg gac agc gat ggc agc acc gac ctg atc ctc att ggg gcc ccc	1439
Asp Val Asp Ser Asp Gly Ser Thr Asp Leu Ile Leu Ile Gly Ala Pro	
465 470 475	
cat tac tat gag cag acc cga ggg ggc cag gtg tcc gtg tgt ccc ttg	1487
His Tyr Tyr Glu Gln Thr Arg Gly Gln Val Ser Val Cys Pro Leu	
480 485 490 495	
cct agg ggg cag agg gtg cag tgg cag tgt gac gct gtt ctc cgt ggt	1535
Pro Arg Gly Gln Arg Val Gln Trp Gln Cys Asp Ala Val Leu Arg Gly	
500 505 510	
gag cag ggc cac ccc tgg ggc cgc ttt ggg gca gcc ctg aca gtg ttg	1583
Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu	
515 520 525	
ggg gat gtg aat gag gac aag ctg ata gac gtg gcc att ggg gcc ccg	1631
Gly Asp Val Asn Glu Asp Lys Leu Ile Asp Val Ala Ile Gly Ala Pro	
530 535 540	
gga gag cag gag aac cgg ggt gct gtc tac ctg ttt cac gga gcc tca	1679
Gly Glu Gln Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Ala Ser	
545 550 555	
gaa tcc ggc atc agc ccc tcc cac agc cag cgg att gcc agc tcc cag	1727
Glu Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Ser Ser Gln	
560 565 570 575	
ctc tcc ccc agg ctg cag tat ttt ggg cag gcg ctg agt ggg ggt cag	1775
Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln	
580 585 590	
gac ctc acc cag gat gga ctg atg gac ctg gcc gtg ggg gcc cgg ggc	1823
Asp Leu Thr Gln Asp Gly Leu Met Asp Leu Ala Val Gly Ala Arg Gly	
595 600 605	
cag gtg ctc ctg ctc agg agt ctg ccg gtg ctg aaa gtg ggg gtg gcc	1871
Gln Val Leu Leu Leu Arg Ser Leu Pro Val Leu Lys Val Gly Val Ala	
610 615 620	
atg aga ttc agc cct gtg gag gtg gcc aag gct gtg tac cgg tgc tgg	1919
Met Arg Phe Ser Pro Val Glu Val Ala Lys Ala Val Tyr Arg Cys Trp	
625 630 635	

gaa gag aag ccc agt gcc ctg gaa gct ggg gac gcc acc gtc tgt ctc Glu Glu Lys Pro Ser Ala Leu Glu Ala Gly Asp Ala Thr Val Cys Leu 640 645 650 655	1967
acc atc cag aaa agc tca ctg gac cag cta ggt gac atc caa agc tct Thr Ile Gln Lys Ser Ser Leu Asp Gln Leu Gly Asp Ile Gln Ser Ser 660 665 670	2015
gtc agg ttt gat ctg gca ctg gac cca ggt cgt ctg act tct cgt gcc Val Arg Phe Asp Leu Ala Leu Asp Pro Gly Arg Leu Thr Ser Arg Ala 675 680 685	2063
att ttc aat gaa acc aag aac ccc act ttg act cga aga aaa acc ctg Ile Phe Asn Glu Thr Lys Asn Pro Thr Leu Thr Arg Arg Lys Thr Leu 690 695 700	2111
gga ctg ggg att cac tgt gaa acc ctg aag ctg ctt ttg cca gat tgt Gly Leu Gly Ile His Cys Glu Thr Leu Lys Leu Leu Pro Asp Cys 705 710 715	2159
gtg gag gat gtg gtg agc ccc atc att ctg cac ctc aac ttc tca ctg Val Glu Asp Val Val Ser Pro Ile Ile Leu His Leu Asn Phe Ser Leu 720 725 730 735	2207
gtg aga gag ccc atc ccc tcc ccc cag aac ctg cgt cct gtg ctg gcc Val Arg Glu Pro Ile Pro Ser Pro Gln Asn Leu Arg Pro Val Leu Ala 740 745 750	2255
gtg ggc tca caa gac ctc ttc act gct tct ctc ccc ttc gag aag aac Val Gly Ser Gln Asp Leu Phe Thr Ala Ser Leu Pro Phe Glu Lys Asn 755 760 765	2303
tgt ggg caa gat ggc ctc tgt gaa ggg gac ctg ggt gtc acc ctc agc Cys Gly Gln Asp Gly Leu Cys Glu Gly Asp Leu Gly Val Thr Leu Ser 770 775 780	2351
ttc tca ggc ctg cag acc ctg acc gtg ggg agc tcc ctg gag ctc aac Phe Ser Gly Leu Gln Thr Leu Thr Val Gly Ser Ser Leu Glu Leu Asn 785 790 795	2399
gtg att gtg act gtg tgg aac gca ggt gag gat tcc tac gga acc gtg Val Ile Val Thr Val Trp Asn Ala Gly Glu Asp Ser Tyr Gly Thr Val 800 805 810 815	2447
gtc agc ctc tac tat cca gca ggg ctg tcc cac cga cgg gtg tca gga Val Ser Leu Tyr Tyr Pro Ala Gly Leu Ser His Arg Arg Val Ser Gly 820 825 830	2495
gcc cag aag cag ccc cat cag agt gcc ctg cgc ctg gca tgt gag aca Ala Gln Lys Gln Pro His Gln Ser Ala Leu Arg Leu Ala Cys Glu Thr 835 840 845	2543
gtg ccc act gag gat gag ggc cta aga agc agc cgc tgc agt gtc aac Val Pro Thr Glu Asp Glu Gly Leu Arg Ser Ser Arg Cys Ser Val Asn 850 855 860	2591
cac ccc atc ttc cat gag ggc tct aac ggc acc ttc ata gtc aca ttc His Pro Ile Phe His Glu Gly Ser Asn Gly Thr Phe Ile Val Thr Phe 865 870 875	2639

gat gtc tcc tac aag gcc acc ctg gga gac agg atg ctt atg agg gcc	2687
Asp Val Ser Tyr Lys Ala Thr Leu Gly Asp Arg Met Leu Met Arg Ala	
880 885 890 895	
agt gca agc agt gag aac aat aag gct tca agc agc aag gcc acc ttc	2735
Ser Ala Ser Ser Glu Asn Asn Lys Ala Ser Ser Lys Ala Thr Phe	
900 905 910	
cag ctg gag ctc ccg gtg aag tat gca gtc tac acc atg atc agc agg	2783
Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Thr Met Ile Ser Arg	
915 920 925	
cag gaa gaa tcc acc aag tac ttc aac ttt gca acc tcc gat gag aag	2831
Gln Glu Glu Ser Thr Lys Tyr Phe Asn Phe Ala Thr Ser Asp Glu Lys	
930 935 940	
aaa atg aaa gag gct gag cat cga tac cgt gtg aat aac ctc agc cag	2879
Lys Met Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Gln	
945 950 955	
cga gat ctg gcc atc agc att aac ttc tgg gtt cct gtc ctg ctg aac	2927
Arg Asp Leu Ala Ile Ser Ile Asn Phe Trp Val Pro Val Leu Leu Asn	
960 965 970 975	
ggg gtg gct gtg tgg gat gtg gtc atg gag gcc cca tct cag agt ctc	2975
Gly Val Ala Val Trp Asp Val Val Met Glu Ala Pro Ser Gln Ser Leu	
980 985 990	
ccc tgt gtt tca gag aga aaa cct ccc cag cat tct gac ttc ctg acc	3023
Pro Cys Val Ser Glu Arg Lys Pro Pro Gln His Ser Asp Phe Leu Thr	
995 1000 1005	
cag att tca aga agt ccc atg ctg gac tgc tcc att gct gac tgc	3068
Gln Ile Ser Arg Ser Pro Met Leu Asp Cys Ser Ile Ala Asp Cys	
1010 1015 1020	
ctg cag ttc cgc tgt gac gtc ccc tcc ttc agc gtc cag gag gag	3113
Leu Gln Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln Glu Glu	
1025 1030 1035	
ctg gat ttc acc ctg aag ggc aat ctc agt ttc ggc tgg gtc cgc	3158
Leu Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val Arg	
1040 1045 1050	
gag aca ttg cag aag aag gtg ttg gtc gtg agt gtg gct gaa att	3203
Glu Thr Leu Gln Lys Lys Val Leu Val Val Ser Val Ala Glu Ile	
1055 1060 1065	
acg ttc gac aca tcc gtg tac tcc cag ctt cca gga cag gag gca	3248
Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala	
1070 1075 1080	
ttt atg aga gct cag atg gag atg gtg cta gaa gaa gac gag gtc	3293
Phe Met Arg Ala Gln Met Glu Met Val Leu Glu Glu Asp Glu Val	
1085 1090 1095	
tac aat gcc att ccc atc atc atg ggc agc tct gtg ggg gct ctg	3338
Tyr Asn Ala Ile Pro Ile Ile Met Gly Ser Ser Val Gly Ala Leu	
1100 1105 1110	

6/11

ctc	ctg	ctg	gcg	ctc	atc	aca	gcc	aca	ctg	tac	aag	ctt	ggc	ttc	3383
Leu	Leu	Leu	Ala	Leu	Ile	Thr	Ala	Thr	Leu	Tyr	Lys	Leu	Gly	Phe	
1115							1120					1125			
ttc	aaa	cgc	cac	tac	aag	gaa	atg	ctg	gag	gac	aag	cct	gaa	gac	3428
Phe	Lys	Arg	His	Tyr	Lys	Glu	Met	Leu	Glu	Asp	Lys	Pro	Glu	Asp	
1130							1135					1140			
act	gcc	aca	ttc	agt	ggg	gac	gat	ttc	agc	tgt	gtg	gcc	cca	aat	3473
Thr	Ala	Thr	Phe	Ser	Gly	Asp	Asp	Phe	Ser	Cys	Val	Ala	Pro	Asn	
1145							1150					1155			
gtg	cct	ttg	tcc	taataatcca	ctttcctgtt	tatctctacc	actgtggcct								3525
Val	Pro	Leu	Ser												
1160															
ggacttgctt	gcaaccataa	atcaacttac	atggaaacaa	cttctgcata	gatctgcact										3585
ggcctaagca	acctaccagg	tgctaagcac	cttctcgag	agatagagat	tgtaatgttt										3645
ttacatatct	gtccatcttt	ttcagcaatg	acccactttt	tacagaagca	ggcatggc										3705
cacgataaaat	tttcatatgc	t													3726

<210> 2
 <211> 1161
 <212> PRT
 <213> Homo sapiens

<400> 2

Thr Phe Gly Thr Val Leu Leu Ser Val Leu Ala Ser Tyr His Gly
 1 5 10 15

Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala Gly
 20 25 30

Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg Leu Val Val
 35 40 45

Gly Ala Pro Leu Glu Val Val Ala Ala Asn Gln Thr Gly Arg Leu Tyr
 50 55 60

Asp Cys Ala Ala Ala Thr Gly Met Cys Gln Pro Ile Pro Leu His Ile
 65 70 75 80

Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala Ser
 85 90 95

Thr Asn Gly Ser Arg Leu Leu Ala Cys Gly Pro Thr Leu His Arg Val
 100 105 110

Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu Leu Gly Ser
 115 120 125

Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro Glu Cys Pro
130 135 140

His Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile
145 150 155 160

Asp Gln Asn Asp Phe Asn Gln Met Lys Gly Phe Val Gln Ala Val Met
165 170 175

Gly Gln Phe Glu Gly Thr Asp Thr Leu Phe Ala Leu Met Gln Tyr Ser
180 185 190

Asn Leu Leu Lys Ile His Phe Thr Phe Thr Gln Phe Arg Thr Ser Pro
195 200 205

Ser Gln Gln Ser Leu Val Asp Pro Ile Val Gln Leu Lys Gly Leu Thr
210 215 220

Phe Thr Ala Thr Gly Ile Leu Thr Val Val Thr Gln Leu Phe His His
225 230 235 240

Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile Val Ile Thr
245 250 255

Asp Gly Gln Lys Tyr Lys Asp Pro Leu Glu Tyr Ser Asp Val Ile Pro
260 265 270

Gln Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly His
275 280 285

Ala Phe Gln Gly Pro Thr Ala Arg Gln Glu Leu Asn Thr Ile Ser Ser
290 295 300

Ala Pro Pro Gln Asp His Val Phe Lys Val Asp Asn Phe Ala Ala Leu
305 310 315 320

Gly Ser Ile Gln Lys Gln Leu Gln Glu Lys Ile Tyr Ala Val Glu Gly
325 330 335

Thr Gln Ser Arg Ala Ser Ser Ser Phe Gln His Glu Met Ser Gln Glu
340 345 350

Gly Phe Ser Thr Ala Leu Thr Met Asp Gly Leu Phe Leu Gly Ala Val
355 360 365

Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn Met
370 375 380

Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg Asp
385 390 395 400

Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly Val Gln
405 410 415

Asn Leu Val Leu Gly Ala Pro Arg Tyr Gln His Thr Gly Lys Ala Val
420 425 430

Ile Phe Thr Gln Val Ser Arg Gln Trp Arg Lys Lys Ala Glu Val Thr
435 440 445

Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val Asp
450 455 460

Val Asp Ser Asp Gly Ser Thr Asp Leu Ile Leu Ile Gly Ala Pro His
465 470 475 480

Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu Pro
485 490 495

Arg Gly Gln Arg Val Gln Trp Gln Cys Asp Ala Val Leu Arg Gly Glu
500 505 510

Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu Gly
515 520 525

Asp Val Asn Glu Asp Lys Leu Ile Asp Val Ala Ile Gly Ala Pro Gly
530 535 540

Glu Gln Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Ala Ser Glu
545 550 555 560

Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Ser Ser Gln Leu
565 570 575

Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln Asp
580 585 590

Leu Thr Gln Asp Gly Leu Met Asp Leu Ala Val Gly Ala Arg Gly Gln
595 600 605

Val Leu Leu Leu Arg Ser Leu Pro Val Leu Lys Val Gly Val Ala Met
610 615 620

Arg Phe Ser Pro Val Glu Val Ala Lys Ala Val Tyr Arg Cys Trp Glu
625 630 635 640

Glu Lys Pro Ser Ala Leu Glu Ala Gly Asp Ala Thr Val Cys Leu Thr
645 650 655

Ile Gln Lys Ser Ser Leu Asp Gln Leu Gly Asp Ile Gln Ser Ser Val
660 665 670

Arg Phe Asp Leu Ala Leu Asp Pro Gly Arg Leu Thr Ser Arg Ala Ile
675 680 685

Phe Asn Glu Thr Lys Asn Pro Thr Leu Thr Arg Arg Lys Thr Leu Gly
690 695 700

Leu Gly Ile His Cys Glu Thr Leu Lys Leu Leu Leu Pro Asp Cys Val
705 710 715 720

Glu Asp Val Val Ser Pro Ile Ile Leu His Leu Asn Phe Ser Leu Val
725 730 735

Arg Glu Pro Ile Pro Ser Pro Gln Asn Leu Arg Pro Val Leu Ala Val
740 745 750

Gly Ser Gln Asp Leu Phe Thr Ala Ser Leu Pro Phe Glu Lys Asn Cys
755 760 765

Gly Gln Asp Gly Leu Cys Glu Gly Asp Leu Gly Val Thr Leu Ser Phe
770 775 780

Ser Gly Leu Gln Thr Leu Thr Val Gly Ser Ser Leu Glu Leu Asn Val
785 790 795 800

Ile Val Thr Val Trp Asn Ala Gly Glu Asp Ser Tyr Gly Thr Val Val
805 810 815

Ser Leu Tyr Tyr Pro Ala Gly Leu Ser His Arg Arg Val Ser Gly Ala
820 825 830

Gln Lys Gln Pro His Gln Ser Ala Leu Arg Leu Ala Cys Glu Thr Val
835 840 845

Pro Thr Glu Asp Glu Gly Leu Arg Ser Ser Arg Cys Ser Val Asn His
850 855 860

Pro Ile Phe His Glu Gly Ser Asn Gly Thr Phe Ile Val Thr Phe Asp
865 870 875 880

Val Ser Tyr Lys Ala Thr Leu Gly Asp Arg Met Leu Met Arg Ala Ser
885 890 895

Ala Ser Ser Glu Asn Asn Lys Ala Ser Ser Ser Lys Ala Thr Phe Gln
900 905 910

Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Thr Met Ile Ser Arg Gln
915 920 925

Glu Glu Ser Thr Lys Tyr Phe Asn Phe Ala Thr Ser Asp Glu Lys Lys
930 935 940

Met Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Gln Arg
945 950 955 960

Asp Leu Ala Ile Ser Ile Asn Phe Trp Val Pro Val Leu Leu Asn Gly
965 970 975

Val Ala Val Trp Asp Val Val Met Glu Ala Pro Ser Gln Ser Leu Pro
980 985 990

Cys Val Ser Glu Arg Lys Pro Pro Gln His Ser Asp Phe Leu Thr Gln
995 1000 1005

Ile Ser Arg Ser Pro Met Leu Asp Cys Ser Ile Ala Asp Cys Leu
1010 1015 1020

Gln Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln Glu Glu Leu
1025 1030 1035

Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val Arg Glu
1040 1045 1050

Thr Leu Gln Lys Lys Val Leu Val Val Ser Val Ala Glu Ile Thr
1055 1060 1065

Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe
1070 1075 1080

Met Arg Ala Gln Met Glu Met Val Leu Glu Glu Asp Glu Val Tyr
1085 1090 1095

Asn Ala Ile Pro Ile Ile Met Gly Ser Ser Val Gly Ala Leu Leu
1100 1105 1110

11/11

Leu Leu Ala Leu Ile Thr Ala Thr Leu Tyr Lys Leu Gly Phe Phe
1115 1120 1125

Lys Arg His Tyr Lys Glu Met Leu Glu Asp Lys Pro Glu Asp Thr
1130 1135 1140

Ala Thr Phe Ser Gly Asp Asp Phe Ser Cys Val Ala Pro Asn Val
1145 1150 1155

Pro Leu Ser
1160